



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gillespie, Alison
Claeps, Brian O.
Chavez-Noriega, Laura Elena
Siegel, Robert
Elliott, Kathryn J.
- (ii) TITLE OF INVENTION: DNA ENCODING HUMAN α AND β SUBUNITS
OF NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR, CELLS TRANSFORMED THEREWITH,
AND RECOMBINANT CELL LINE EXPRESSING
A HUMAN α AND β SUBUNITS OF NEURONAL
NICOTINIC ACETYLCHOLINE RECEPTOR
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merck & Co., Inc.
 - (B) STREET: 126 E. Lincoln Avenue
 - (C) CITY: Rahway
 - (D) STATE: NJ
 - (E) COUNTRY: USA
 - (F) ZIP: 07065-0907
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/703,951
 - (B) FILING DATE: 01-NOV-2000
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/487,596
 - (B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO US94/02447
 - (B) FILING DATE: 08-MAR-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/149,503
 - (B) FILING DATE: 08-NOV-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/028,031
 - (B) FILING DATE: 08-MAR-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/938,154
 - (B) FILING DATE: 30-NOV-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/504,455

(B) FILING DATE: 03-APR-1990

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kohli, Vineet
 (B) REGISTRATION NUMBER: 37,003
 (C) REFERENCE/DOCKET NUMBER: SD9951IA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 732-594-3889
 (B) TELEFAX: 732-594-4720

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 166..1755
 (D) OTHER INFORMATION: /product= "ALPHA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAATGACCTG TTTTCTTCTG TAACCACAGG TTCGGTGGTG AGAGGAASCY TCGCAGAATC	60
CAGCAGAATC CTCACAGAAT CCAGCAGCAG CTCTGCTGGG GACATGGTCC ATGGTGCAAC	120
CCACAGCAAA GCCCTGACCT GACCTCCTGA TGCTCAGGAG AAGCCATGGG CCCCTCCTGT	180
CCTGTGTTCC TGTCTTTCAC AAAGCTCAGC CTGTGGTGGC TCCTTCTGAC CCCAGCAGGT	240
GGAGAGGAAG CTAAGCGCCC ACCTCCCAGG GCTCCTGGAG ACCCACTCTC CTCTCCCAGT	300
CCCACGGCAT TGCCGCAGGG AGGCTCGCAT ACCGAGACTG AGGACCGGCT CTTCAAACAC	360
CTCTTCCGGG GCTACAACCG CTGGGCGCGC CCGGTGCCCA AACTTTCAGA CGTGGTGATT	420
GTGCGCTTTG GACTGTCCAT CGCTCAGCTC ATCGATGTGG ATGAGAAGAA CCAAATGATG	480
ACCACCAACG TCTGGCTAAA ACAGGAGTGG AGCGACTACA AACTGCGCTG GAACCCCGCT	540
GATTTTGGCA ACATCACATC TCTCAGGGTC CCTTCTGAGA TGATCTGGAT CCCCACATT	600
GTCTCTTACA ACAATGCAGA TGGGGAGTTT GCAGTGACCC ACATGACCAA GGCCCACCTC	660
TTCTCCACGG GCACTGTGCA CTGGGTGCCC CCGGCCATCT ACAAGAGCTC CTGCAGCATC	720
GACGTCACCT TCTTCCCCTT CGACCAGCAG AACTGCAAGA TGAAGTTTGG CTCCTGGACT	780
TATGACAAGG CCAAGATCGA CCTGGAGCAG ATGGAGCAGA CTGTGGACCT GAAGGACTAC	840
TGGGAGAGCG GCGAGTGGGC CATCGTCAAT GCCACGGGCA CCTACAACAG CAAGAAGTAC	900
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ACCGTCTTCG TGCTCAATGT GCACCACCGC TCCCCCAGCA CCCACACCAT GCCCCACTGG      1260
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CCCGTGGAGC TCTGCCACCC CCTACGCCTG AAGCTCAGCC CCTCTTATCA CTGGCTGGAG      1380
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AGTAATAAGG GCTCTTCCGG AAGGGGAGGA AGCGGGAGGC AGGGCCTGCA CCTGATGTGG      2040
AGGTACAGGG CAGATCTTCC CTACCGGGGA GGGATGGATG GTTGGATACA GGTGGCTGGG      2100
CTATTCCATC CATCTGGAAG CACATTTGAG CCTCCAGGCT TCTCCTTGAC GTCATTCCCTC      2160
TCCTTCCTTG CTCCAAAATG GCTCTGCACC AGCCGGCCCC CAGGAGGTCT GGCAGAGCTG      2220
AGAGCCATGG CCTGCAGGGG CTCCATATGT CCCTACGCGT GCAGCAGGCA AACAAGA      2277

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Pro Ser Cys Pro Val Phe Leu Ser Phe Thr Lys Leu Ser Leu
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Trp Trp Leu Leu Leu Thr Pro Ala Gly Gly Glu Glu Ala Lys Arg Pro

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20					25					30					
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		35					40					45			
Leu	Pro	Gln	Gly	Gly	Ser	His	Thr	Glu	Thr	Glu	Asp	Arg	Leu	Phe	Lys
	50					55					60				
His	Leu	Phe	Arg	Gly	Tyr	Asn	Arg	Trp	Ala	Arg	Pro	Val	Pro	Asn	Thr
65					70					75					80
Ser	Asp	Val	Val	Ile	Val	Arg	Phe	Gly	Leu	Ser	Ile	Ala	Gln	Leu	Ile
				85					90					95	
Asp	Val	Asp	Glu	Lys	Asn	Gln	Met	Met	Thr	Thr	Asn	Val	Trp	Leu	Lys
			100					105					110		
Gln	Glu	Trp	Ser	Asp	Tyr	Lys	Leu	Arg	Trp	Asn	Pro	Ala	Asp	Phe	Gly
		115					120					125			
Asn	Ile	Thr	Ser	Leu	Arg	Val	Pro	Ser	Glu	Met	Ile	Trp	Ile	Pro	Asp
	130					135					140				
Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Glu	Phe	Ala	Val	Thr	His	Met
145						150					155				160
Thr	Lys	Ala	His	Leu	Phe	Ser	Thr	Gly	Thr	Val	His	Trp	Val	Pro	Pro
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Asp	Gln	Gln	Asn	Cys	Lys	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Lys
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Ala	Lys	Ile	Asp	Leu	Glu	Gln	Met	Glu	Gln	Thr	Val	Asp	Leu	Lys	Asp
	210					215					220				
Tyr	Trp	Glu	Ser	Gly	Glu	Trp	Ala	Ile	Val	Asn	Ala	Thr	Gly	Thr	Tyr
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			260					265					270		
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		275					280						285		
Leu	Pro	Ser	Asp	Cys	Gly	Glu	Lys	Ile	Thr	Leu	Cys	Ile	Ser	Val	Leu
	290					295					300				
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305					310						315				320
Thr	Ser	Leu	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Thr	Met
				325					330					335	
Ile	Phe	Val	Thr	Leu	Ser	Ile	Val	Ile	Thr	Val	Phe	Val	Leu	Asn	Val
			340					345					350		

His His Arg Ser Pro Ser Thr His Thr Met Pro His Trp Val Arg Gly
 355 360 365
 Ala Leu Leu Gly Cys Val Pro Arg Trp Leu Leu Met Asn Arg Pro Pro
 370 375 380
 Pro Pro Val Glu Leu Cys His Pro Leu Arg Leu Lys Leu Ser Pro Ser
 385 390 395 400
 Tyr His Trp Leu Glu Ser Asn Val Asp Ala Glu Glu Arg Glu Val Val
 405 410 415
 Val Glu Glu Glu Asp Arg Trp Ala Cys Ala Gly His Val Ala Pro Ser
 420 425 430
 Val Gly Thr Leu Cys Ser His Gly His Leu His Ser Gly Ala Ser Gly
 435 440 445
 Pro Lys Ala Glu Ala Leu Leu Gln Glu Gly Glu Leu Leu Leu Ser Pro
 450 455 460
 His Met Gln Lys Ala Leu Glu Gly Val His Tyr Ile Ala Asp His Leu
 465 470 475 480
 Arg Ser Glu Asp Ala Asp Ser Ser Val Lys Glu Asp Trp Lys Tyr Val
 485 490 495
 Ala Met Val Ile Asp Arg Ile Phe Leu Trp Leu Phe Ile Ile Val Cys
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 515 520 525
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 39..1553
- (D) OTHER INFORMATION: /product= "ALPHA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCAGGGCCTC AGAGGCTGAG CACCGTCTAT TTGAGCGGCT GTTTGAAGAT TACAATGAGA	180

TCATCCGGCC	TGTAGCCAAC	GTGTCTGACC	CAGTCATCAT	CCATTTTCGAG	GTGTCCATGT	240
CTCAGCTGGT	GAAGGTGGAT	GAAGTAAACC	AGATCATGGA	GACCAACCTG	TGGCTCAAGC	300
AAATCTGGAA	TGACTACAAG	CTGAAGTGA	ACCCCTCTGA	CTATGGTGGG	GCAGAGTTCA	360
TGCGTGTC	TGCACAGAAG	ATCTGGAAGC	CAGACATTGT	GCTGTATAAC	AATGCTGTTG	420
GGGATTTCCA	GGTGGACGAC	AAGACCAAAG	CCTTACTCAA	GTACACTGGG	GAGGTGACTT	480
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TGGTCCTGAT	CGGCTCTTCC	ATGAACCTCA	AGGACTATTG	GGAGAGCGGC	GAGTGGGCCA	660
TCATCAAAGC	CCCAGGCTAC	AAACACGACA	TCAAGTACAG	CTGCTGCGAG	GAGATCTACC	720
CCGACATCAC	ATACTCGCTG	WWCATCCGGC	GGCTGTCGTT	GTTCTACACC	ATCAWCCTCA	780
TCATCCGCTG	GCTGATCATC	TCCTTCATCA	CTGTGGTCGT	CTCCTACCTG	CCCTCCGACT	840
GCGGCGAGAA	GGTGACCCTG	TGYATTTCTG	TCCTCCTCTC	CCTGACGGTG	TTTCTCCTGG	900
TGATCACTGA	GACCATCCCT	TCCACCTCGC	TGGTCATCCC	CCTGATTGGA	GAGTACCTCC	960
TGWWCACCAT	GATTTGTGTA	ACCTTGTTCA	TCGACATCAC	CGTCTGCGTG	CTCAACGTGC	1020
ACTACAGAAC	CCCGACGACA	CACACAATGC	CCTCATGGGT	GAAGACTGTA	TTCTTGAMCC	1080
TGCTCCCCAG	GGTCATGTWC	ATGACCAGGC	CAACAAGCAA	CGAGGGCAAC	GCTCAGAAGC	1140
CGAGGCCCCCT	CTACGGTGCC	GAGCTCTCAA	ATCTGAATTG	CTTCAGCCGC	GCAGAGTCCA	1200
AAGGCTGCAA	GGAGGGCTAC	CCCTGCCAGG	ACGGGATGTG	TGGTTACTGC	CACCACCGCA	1260
GGATAAAAAT	CTCCAATTTT	AGTGCTAACC	TCACGAGAAG	CTCTAGTTCT	GAATCTGTTG	1320
ATGCTGTGCT	GTCCTCTCT	GCTTTGTCAC	CAGAAATCAA	AGAAGCCATC	CAAAGTGTC	1380
AGTATATTGC	TGAAAATATG	AAAGCACAAA	ATGAAGCCAA	AGAGATTCAA	GATGATTGGA	1440
AGTATGTTGC	CATGGTGATT	GATCGTATTT	TTCTGTGGGT	TTTCACCCTG	GTGTGCATTC	1500
TAGGGACAGC	AGGATTGTTT	CTGCAACCCC	TGATGGCCAG	GGAAGATGCA	TAAGCACTAA	1560
GCTGTGTGCC	TGCCTGGGAG	ACTTCCTTGT	GTCAGGGCAG	GAGGAGGCTG	CTTCCTAGTA	1620
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met 1	Gly	Ser	Gly	Pro 5	Leu	Ser	Leu	Pro	Leu 10	Ala	Leu	Ser	Pro	Pro	Arg 15
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Ala	Glu	His 35	Arg	Leu	Phe	Glu	Arg 40	Leu	Phe	Glu	Asp	Tyr 45	Asn	Glu	Ile
Ile	Arg 50	Pro	Val	Ala	Asn	Val 55	Ser	Asp	Pro	Val	Ile	Ile	His	Phe	Glu
Val 65	Ser	Met	Ser	Gln 70	Leu	Val	Lys	Val	Asp	Glu 75	Val	Asn	Gln	Ile	Met 80
Glu	Thr	Asn	Leu	Trp 85	Leu	Lys	Gln	Ile	Trp 90	Asn	Asp	Tyr	Lys	Leu 95	Lys
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Gln	Lys	Ile 115	Trp	Lys	Pro	Asp	Ile 120	Val	Leu	Tyr	Asn	Asn	Ala	Val	Gly
Asp	Phe 130	Gln	Val	Asp	Asp	Lys 135	Thr	Lys	Ala	Leu	Leu 140	Lys	Tyr	Thr	Gly
Glu 145	Val	Thr	Trp	Ile	Pro 150	Pro	Ala	Ile	Phe	Lys 155	Ser	Ser	Cys	Lys	Ile 160
Asp	Val	Thr	Tyr	Phe 165	Pro	Phe	Asp	Tyr	Gln 170	Asn	Cys	Thr	Met	Lys 175	Phe
Gly	Ser	Trp	Ser 180	Tyr	Asp	Lys	Ala	Lys 185	Ile	Asp	Leu	Val	Leu 190	Ile	Gly
Ser	Ser	Met 195	Asn	Leu	Lys	Asp	Tyr 200	Trp	Glu	Ser	Gly	Glu 205	Trp	Ala	Ile
Ile	Lys 210	Ala	Pro	Gly	Tyr	Lys 215	His	Asp	Ile	Lys	Tyr 220	Ser	Cys	Cys	Glu
Glu 225	Ile	Tyr	Pro	Asp	Ile 230	Thr	Tyr	Ser	Leu	Xaa 235	Ile	Arg	Arg	Leu	Ser 240
Leu	Phe	Tyr	Thr	Ile 245	Xaa	Leu	Ile	Ile	Arg 250	Trp	Leu	Ile	Ile	Ser 255	Phe
Ile	Thr	Val	Val 260	Val	Ser	Tyr	Leu	Pro 265	Ser	Asp	Cys	Gly	Glu 270	Lys	Val
Thr	Leu	Cys 275	Ile	Ser	Val	Leu	Leu 280	Ser	Leu	Thr	Val	Phe 285	Leu	Leu	Val
Ile	Thr 290	Glu	Thr	Ile	Pro	Ser 295	Thr	Ser	Leu	Val	Ile 300	Pro	Leu	Ile	Gly
Glu 305	Tyr	Leu	Leu	Xaa 310	Thr	Met	Ile	Cys	Val	Thr 315	Leu	Ser	Ile	Asp	Ile 320
Thr	Val	Cys	Val	Leu	Asn	Val	His	Tyr	Arg	Thr	Pro	Thr	Thr	His	Thr

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Arg	Pro	Leu	Tyr	Gly	Ala	Glu	Leu	Ser	Asn	Leu	Asn	Cys	Phe	Ser	Arg	
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Ala	Glu	Ser	Lys	Gly	Cys	Lys	Glu	Gly	Tyr	Pro	Cys	Gln	Asp	Gly	Met	
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Cys	Gly	Tyr	Cys	His	His	Arg	Arg	Ile	Lys	Ile	Ser	Asn	Phe	Ser	Ala	
				405					410					415		
Asn	Leu	Thr	Arg	Ser	Ser	Ser	Ser	Glu	Ser	Val	Asp	Ala	Val	Leu	Ser	
			420					425					430			
Leu	Ser	Ala	Leu	Ser	Pro	Glu	Ile	Lys	Glu	Ala	Ile	Gln	Ser	Val	Lys	
		435					440					445				
Tyr	Ile	Ala	Glu	Asn	Met	Lys	Ala	Gln	Asn	Glu	Ala	Lys	Glu	Ile	Gln	
	450					455					460					
Asp	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val	Ile	Asp	Arg	Ile	Phe	Leu	Trp	
465					470					475					480	
Val	Phe	Thr	Leu	Val	Cys	Ile	Leu	Gly	Thr	Ala	Gly	Leu	Phe	Leu	Gln	
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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 173..2056
- (D) OTHER INFORMATION: /product= "ALPHA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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CGGCGGGGAG	CCGGGAGCCG	CCCGCATCTA	GAGCCCCGGA	GGTGCGTGCG	CCATGGAGCT	180
AGGGGGCCCC	GGAGCGCCGC	GGCTGCTGCC	GCCGCTGCTG	CTGCTTCTGG	GGACCGGCCT	240

CCTGCGCGCC	AGCAGCCATG	TGGAGACCCG	GGCCCACGCC	GAGGAGCGGC	TCCTGAAGAA	300
ACTCTTCTCC	GGTTACAACA	AGTGGTCCCG	ACCCGTGGCC	AACATCTCGG	ACGTGGTCCCT	360
CGTCCGCTTC	GGCCTGTCCA	TCGCTCAGCT	CATTGACGTG	GATGAGAAGA	ACCAGATGAT	420
GACCACGAAC	GTCTGGGTGA	AGCAGGAGTG	GCACGACTAC	AAGCTGCGCT	GGGACCCAGC	480
TGACTATGAG	AATGTCACCT	CCATCCGCAT	CCCCTCCGAG	CTCATCTGGC	GGCCGGACAT	540
CGCCCTCTAC	AACAATGCTG	ACGGGGACTT	CGCGGCCACC	CACCTGACCA	AGGCCCACCT	600
GTTCCATGAC	GGGCGGGTGC	AGCGGACTCC	CCCGGCCATT	TACAAGAGCT	CCTGCAGCAT	660
CGACGTCACC	TTCTTCCCCT	TCGACCAGCA	GAAGTGCACC	ATGAAATTCTG	GCTCCTGGAC	720
CTACGACAAG	GCCAAGATCG	ACCTGGTGAA	CATGCACAGC	CGCGTGGACC	AGCTGGACTT	780
CTGGGAGAGT	GGCGAGTGGC	TCATCTCGGA	CGCCGTGGGC	ACCTACAACA	CCAGGAAGTA	840
CGAGTGCTGC	GCCGAGATCT	ACCCGGACAT	CACCTATGCC	TACGCCATCC	GGCGGCTGCC	900
GCTCTTCTAC	ACCATCAACC	TCATCATCCC	CTGGCTGCTC	ATCTCCTGCC	TCACCGCGCT	960
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GTCGCTCACC	GTCTTCCTGC	TGCTCATCAC	CGAGATCATC	CCGTCCACCT	CACTGGTCAT	1080
CCCCTCATC	GGCGAGTACC	TGCTGTTCAC	CATGATCTTC	GTCACCTTGT	CCATCGCCAT	1140
CACGGTCTTC	GTGCTCAACG	TGCACCACCG	CTCGCCACGC	ACGCACACCA	TGCCCACCTG	1200
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GTCACCTTCC	GACCAGCTCC	CTCCTCAGCA	GCCCCCTGAA	GCTGAGAAAG	CCAGCCCCCA	1500
CCCCCTGCCT	GGACCTTGCC	GCCCGCCCCA	CGGCACCCAG	GCACCAGGGC	TGGCCAAAGC	1560
CAGGTCCCTC	AGCGTCCAGC	ACATGTCCAG	CCCTGGCGAA	GCGGTGGAAG	GCGGCGTCCG	1620
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CGCCACGGTC	AAGACCCGCA	GCACCAAAGC	GCCGCCGCCG	CACCTGCCCC	TGTCGCCGGC	1860
CCTGAGCCGG	GCGGTGGAGG	GCGTCCAGTA	CATTGCAGAC	CACCTGAAGG	CCGAAGACAC	1920
AGACTTCTCG	GTGAAGGAGG	ACTGGAAGTA	CGTGCCCATG	GTCATCGACC	GCATCTTCCT	1980
CTGGATGTTC	ATCATCGTCT	GCCTGCTGGG	GACGGTGGGC	CTCTTCCTGC	CGCCCTGGCT	2040
GGCTGGCATG	ATCTAGGAAG	GGACCGGGAG	CCTGCGTGGC	CTGGGGCTGC	CGYGCACGGG	2100

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GCCAGCATCC ATGCGGCCGG CCTGGGGCCG GGCTGGCTTC TCCCTGGACT CTGTGGGGCC      2160
ACACGTTTGC CAAATTTTCC TTCCTGTTCT GTGTCTGCTG TAAGACGGCC TTGGACGGCG      2220
ACACGGCCTC TGGGGAGACC GAGTGTGGAG CTGCTTCCAG TTGGACTCTS GCCTCAGNAG      2280
GCAGCGGCTT GGAGCAGAGG TGGCGGTCGC CGCCTYCTAC CTGCAGGACT CGGGCTAAGT      2340
CCAGCTCTCC CCCTGCGCAG CCC                                              2363

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Glu Leu Gly Gly Pro Gly Ala Pro Arg Leu Leu Pro Pro Leu Leu
 1              5              10              15
Leu Leu Leu Gly Thr Gly Leu Leu Arg Ala Ser Ser His Val Glu Thr
 20              25              30
Arg Ala His Ala Glu Glu Arg Leu Leu Lys Lys Leu Phe Ser Gly Tyr
 35              40              45
Asn Lys Trp Ser Arg Pro Val Ala Asn Ile Ser Asp Val Val Leu Val
 50              55              60
Arg Phe Gly Leu Ser Ile Ala Gln Leu Ile Asp Val Asp Glu Lys Asn
 65              70              75              80
Gln Met Met Thr Thr Asn Val Trp Val Lys Gln Glu Trp His Asp Tyr
 85              90              95
Lys Leu Arg Trp Asp Pro Ala Asp Tyr Glu Asn Val Thr Ser Ile Arg
100              105              110
Ile Pro Ser Glu Leu Ile Trp Arg Pro Asp Ile Ala Leu Tyr Asn Asn
115              120              125
Ala Asp Gly Asp Phe Ala Ala Thr His Leu Thr Lys Ala His Leu Phe
130              135              140
His Asp Gly Arg Val Gln Arg Thr Pro Pro Ala Ile Tyr Lys Ser Ser
145              150              155              160
Cys Ser Ile Asp Val Thr Phe Phe Pro Phe Asp Gln Gln Asn Cys Thr
165              170              175
Met Lys Phe Gly Ser Trp Thr Tyr Asp Lys Ala Lys Ile Asp Leu Val
180              185              190
Asn Met His Ser Arg Val Asp Gln Leu Asp Phe Trp Glu Ser Gly Glu
195              200              205

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Trp Leu Ile Ser Asp Ala Val Gly Thr Tyr Asn Thr Arg Lys Tyr Glu
 210 215 220
 Cys Cys Ala Glu Ile Tyr Pro Asp Ile Thr Tyr Ala Tyr Ala Ile Arg
 225 230 235 240
 Arg Leu Pro Leu Phe Tyr Thr Ile Asn Leu Ile Ile Pro Trp Leu Leu
 245 250 255
 Ile Ser Cys Leu Thr Ala Leu Val Phe Tyr Leu Pro Ser Glu Cys Gly
 260 265 270
 Glu Lys Ile Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe
 275 280 285
 Leu Leu Leu Ile Thr Glu Ile Ile Pro Ser Thr Ser Leu Val Ile Pro
 290 295 300
 Leu Ile Gly Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser
 305 310 315 320
 Ile Ala Ile Thr Val Phe Val Leu Asn Val His His Arg Ser Pro Arg
 325 330 335
 Thr His Thr Met Pro Thr Trp Val Arg Arg Val Phe Leu Asp Ile Val
 340 345 350
 Pro Arg Leu Leu Leu Met Lys Arg Pro Ser Val Val Lys Asp Asn Cys
 355 360 365
 Arg Arg Leu Ile Glu Ser Met His Lys Met Ala Ser Ala Pro Arg Phe
 370 375 380
 Trp Pro Glu Pro Glu Gly Glu Pro Pro Ala Thr Ser Gly Thr Gln Ser
 385 390 395 400
 Leu His Pro Pro Ser Pro Ser Phe Cys Val Pro Leu Asp Val Pro Ala
 405 410 415
 Glu Pro Gly Pro Ser Cys Lys Ser Pro Ser Asp Gln Leu Pro Pro Gln
 420 425 430
 Gln Pro Leu Glu Ala Glu Lys Ala Ser Pro His Pro Ser Pro Gly Pro
 435 440 445
 Cys Arg Pro Pro His Gly Thr Gln Ala Pro Gly Leu Ala Lys Ala Arg
 450 455 460
 Ser Leu Ser Val Gln His Met Ser Ser Pro Gly Glu Ala Val Glu Gly
 465 470 475 480
 Gly Val Arg Cys Arg Ser Arg Ser Ile Gln Tyr Cys Val Pro Arg Asp
 485 490 495
 Asp Ala Ala Pro Glu Ala Asp Gly Gln Ala Ala Gly Ala Leu Ala Ser
 500 505 510
 Arg Asn Ser His Ser Ala Glu Leu Pro Pro Pro Asp Gln Pro Ser Pro
 515 520 525
 Cys Lys Cys Thr Cys Lys Lys Glu Pro Ser Ser Val Ser Pro Ser Ala

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      530              535              540
Thr Val Lys Thr Arg Ser Thr Lys Ala Pro Pro Pro His Leu Pro Leu
545              550              555              560

Ser Pro Ala Leu Ser Arg Ala Val Glu Gly Val Gln Tyr Ile Ala Asp
              565              570              575

His Leu Lys Ala Glu Asp Thr Asp Phe Ser Val Lys Glu Asp Trp Lys
              580              585              590

Tyr Val Ala Met Val Ile Asp Arg Ile Phe Leu Trp Met Phe Ile Ile
              595              600              605

Val Cys Leu Leu Gly Thr Val Gly Leu Phe Leu Pro Pro Trp Leu Ala
              610              615              620

Gly Met Ile
625

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 155..1561
- (D) OTHER INFORMATION: /product= "ALPHA-5 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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CCCCGCGGGA GCTGTGGCGC GGAGCGGCCC CGCTGCTGCG TCTGCCCTCG TTTTGTCTCA      60
CGACTCACAC TCAGTGCTGC ATTCCCCAAG AGTTCGCGTT CCCC GCGCGG CGGTTCGAGAG      120
GCGGCTGCCC GCGGTCCCGC GCGGGCGCGG GGCG ATG GCG GCG CGG GGG TCA      172
                               Met Ala Ala Arg Gly Ser
                               1               5

GGG CCC CGC GCG CTC CGC CTG CTG CTC TTG GTC CAG CTG GTC GCG GGG      220
Gly Pro Arg Ala Leu Arg Leu Leu Leu Val Gln Leu Val Ala Gly
              10              15              20

CGC TGC GGT CTA GCG GGC GCG GCG GGC GGC GCG CAG AGA GGA TTA TCT      268
Arg Cys Gly Leu Ala Gly Ala Ala Gly Gly Ala Gln Arg Gly Leu Ser
              25              30              35

GAA CCT TCT TCT ATT GCA AAA CAT GAA GAT AGT TTG CTT AAG GAT TTA      316
Glu Pro Ser Ser Ile Ala Lys His Glu Asp Ser Leu Leu Lys Asp Leu
              40              45              50

TTT CAA GAC TAC GAA AGA TGG GTT CGT CCT GTG GAA CAC CTG AAT GAC      364
Phe Gln Asp Tyr Glu Arg Trp Val Arg Pro Val Glu His Leu Asn Asp

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55	60	65	70	
AAA ATA AAA ATA AAA TTT GGA CTT GCA ATA TCT CAA TTG GTG GAT GTG Lys Ile Lys Ile Lys Phe Gly Leu Ala Ile Ser Gln Leu Val Asp Val 75 80 85				412
GAT GAG AAA AAT CAG TTA ATG ACA ACA AAC GTC TGG TTG AAA CAG GAA Asp Glu Lys Asn Gln Leu Met Thr Thr Asn Val Trp Leu Lys Gln Glu 90 95 100				460
TGG ATA GAT GTA AAA TTA AGA TGG AAC CCT GAT GAC TAT GGT GGA ATA Trp Ile Asp Val Lys Leu Arg Trp Asn Pro Asp Asp Tyr Gly Gly Ile 105 110 115				508
AAA GTT ATA CGT GTT CCT TCA GAC TCT GTC TGG ACA CCA GAC ATC GTT Lys Val Ile Arg Val Pro Ser Asp Ser Val Trp Thr Pro Asp Ile Val 120 125 130				556
TTG TTT GAT AAT GCA GAT GGA CGT TTT GAA GGG ACC AGT ACG AAA ACA Leu Phe Asp Asn Ala Asp Gly Arg Phe Glu Gly Thr Ser Thr Lys Thr 135 140 145 150				604
GTC ATC AGG TAC AAT GGC ACT GTC ACC TGG ACT CCA CCG GCA AAC TAC Val Ile Arg Tyr Asn Gly Thr Val Thr Trp Thr Pro Pro Ala Asn Tyr 155 160 165				652
AAA AGT TCC TGT ACC ATA GAT GTC ACG TTT TTC CCA TTT GAC CTT CAG Lys Ser Ser Cys Thr Ile Asp Val Thr Phe Phe Pro Phe Asp Leu Gln 170 175 180				700
AAC TGT TCC ATG AAA TTT GGT TCT TGG ACT TAT GAT GGA TCA CAG GTT Asn Cys Ser Met Lys Phe Gly Ser Trp Thr Tyr Asp Gly Ser Gln Val 185 190 195				748
GAT ATA ATT CTA GAG GAC CAA GAT GTA GAC AAG AGA GAT TTT TTT GAT Asp Ile Ile Leu Glu Asp Gln Asp Val Asp Lys Arg Asp Phe Phe Asp 200 205 210				796
AAT GGA GAA TGG GAG ATT GTG AGT GCA ACA GGG AGC AAA GGA AAC AGA Asn Gly Glu Trp Glu Ile Val Ser Ala Thr Gly Ser Lys Gly Asn Arg 215 220 225 230				844
ACC GAC AGC TGT TGC TGG TAT CCG TAT GTC ACT TAC TCA TTT GTA ATC Thr Asp Ser Cys Cys Trp Tyr Pro Tyr Val Thr Tyr Ser Phe Val Ile 235 240 245				892
AAG CGC CTG CCT CTC TTT TAT ACC TTG TTC CTT ATA ATA CCC TGT ATT Lys Arg Leu Pro Leu Phe Tyr Thr Leu Phe Leu Ile Ile Pro Cys Ile 250 255 260				940
GGG CTC TCA TTT TTA ACT GTA CTT GTC TTC TAT CTT CCT TCA AAT GAA Gly Leu Ser Phe Leu Thr Val Leu Val Phe Tyr Leu Pro Ser Asn Glu 265 270 275				988
GGT GAA AAG ATT TGT CTC TGC ACT TCA GTA CTT GTG TCT TTG ACT GTC Gly Glu Lys Ile Cys Leu Cys Thr Ser Val Leu Val Ser Leu Thr Val 280 285 290				1036
TTC CTT CTG GTT ATT GAA GAG ATC ATA CCA TCA TCT TCA AAA GTC ATA Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser Ser Ser Lys Val Ile 295 300 305 310				1084

CCT CTA ATT GGA GAG TAT CTG GTA TTT ACC ATG ATT TTT GTG ACA CTG	1132
Pro Leu Ile Gly Glu Tyr Leu Val Phe Thr Met Ile Phe Val Thr Leu	
315 320 325	
TCA ATT ATG GTA ACC GTC TTC GCT ATC AAC ATT CAT CAT CGT TCT TCC	1180
Ser Ile Met Val Thr Val Phe Ala Ile Asn Ile His His Arg Ser Ser	
330 335 340	
TCA ACA CAT AAT GCC ATG GCG CCT TTG GTC CGC AAG ATA TTT CTT CAC	1228
Ser Thr His Asn Ala Met Ala Pro Leu Val Arg Lys Ile Phe Leu His	
345 350 355	
ACG CTT CCC AAA CTG CTT TGC ATG AGA AGT CAT GTA GAC AGG TAC TTC	1276
Thr Leu Pro Lys Leu Leu Cys Met Arg Ser His Val Asp Arg Tyr Phe	
360 365 370	
ACT CAG AAA GAG GAA ACT GAG AGT GGT AGT GGA CCA AAA TCT TCT AGA	1324
Thr Gln Lys Glu Glu Thr Glu Ser Gly Ser Gly Pro Lys Ser Ser Arg	
375 380 385 390	
AAC ACA TTG GAA GCT GCG CTC AAT TCT ATT CGC TAC ATT ACA AGA CAC	1372
Asn Thr Leu Glu Ala Ala Leu Asn Ser Ile Arg Tyr Ile Thr Arg His	
395 400 405	
ATC ATG AAG GAA AAT GAT GTC CGT GAG GTT GTT GAA GAT TGG AAA TTC	1420
Ile Met Lys Glu Asn Asp Val Arg Glu Val Val Glu Asp Trp Lys Phe	
410 415 420	
ATA GCC CAG GTT CTT GAT CGG ATG TTT CTG TGG ACT TTT CTT TTC GTT	1468
Ile Ala Gln Val Leu Asp Arg Met Phe Leu Trp Thr Phe Leu Phe Val	
425 430 435	
TCA ATT GTT GGA TCT CTT GGG CTT TTT GTT CCT GTT ATT TAT AAA TGG	1516
Ser Ile Val Gly Ser Leu Gly Leu Phe Val Pro Val Ile Tyr Lys Trp	
440 445 450	
GCA AAT ATA TTA ATA CCA GTT CAT ATT GGA AAT GCA AAT AAG TGAAGCCTCC	1568
Ala Asn Ile Leu Ile Pro Val His Ile Gly Asn Ala Asn Lys	
455 460 465	
CAAGGGACTG AAGTATACAT TTAGTTAACA CACATATATC TGATGGCACC TATAAAATTA	1628
TGAAAATGTA AGTTATGTGT TAAATTTAGT GCAAGCTTTA ACAGACTAAG TTGCTAACCT	1688
CAATTTATGT TAACAGATGA TCCATTTGAA CAGTTGGCTG TATGACTGAA GTAATAACTG	1748
ATGAGATACA TTTGATCTTG TAAAAATAGC AAAATATTAT CTGAACTGGA CTAGTGAAAA	1808
ATCTAGTATT TGTATCCTGG	1828

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 468 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Ala	Arg	Gly	Ser	Gly	Pro	Arg	Ala	Leu	Arg	Leu	Leu	Leu	Leu	1	5	10	15
Val	Gln	Leu	Val	Ala	Gly	Arg	Cys	Gly	Leu	Ala	Gly	Ala	Ala	Gly	Gly	20	25	30	
Ala	Gln	Arg	Gly	Leu	Ser	Glu	Pro	Ser	Ser	Ile	Ala	Lys	His	Glu	Asp	35	40	45	
Ser	Leu	Leu	Lys	Asp	Leu	Phe	Gln	Asp	Tyr	Glu	Arg	Trp	Val	Arg	Pro	50	55	60	
Val	Glu	His	Leu	Asn	Asp	Lys	Ile	Lys	Ile	Lys	Phe	Gly	Leu	Ala	Ile	65	70	75	80
Ser	Gln	Leu	Val	Asp	Val	Asp	Glu	Lys	Asn	Gln	Leu	Met	Thr	Thr	Asn	85	90	95	
Val	Trp	Leu	Lys	Gln	Glu	Trp	Ile	Asp	Val	Lys	Leu	Arg	Trp	Asn	Pro	100	105	110	
Asp	Asp	Tyr	Gly	Gly	Ile	Lys	Val	Ile	Arg	Val	Pro	Ser	Asp	Ser	Val	115	120	125	
Trp	Thr	Pro	Asp	Ile	Val	Leu	Phe	Asp	Asn	Ala	Asp	Gly	Arg	Phe	Glu	130	135	140	
Gly	Thr	Ser	Thr	Lys	Thr	Val	Ile	Arg	Tyr	Asn	Gly	Thr	Val	Thr	Trp	145	150	155	160
Thr	Pro	Pro	Ala	Asn	Tyr	Lys	Ser	Ser	Cys	Thr	Ile	Asp	Val	Thr	Phe	165	170	175	
Phe	Pro	Phe	Asp	Leu	Gln	Asn	Cys	Ser	Met	Lys	Phe	Gly	Ser	Trp	Thr	180	185	190	
Tyr	Asp	Gly	Ser	Gln	Val	Asp	Ile	Ile	Leu	Glu	Asp	Gln	Asp	Val	Asp	195	200	205	
Lys	Arg	Asp	Phe	Phe	Asp	Asn	Gly	Glu	Trp	Glu	Ile	Val	Ser	Ala	Thr	210	215	220	
Gly	Ser	Lys	Gly	Asn	Arg	Thr	Asp	Ser	Cys	Cys	Trp	Tyr	Pro	Tyr	Val	225	230	235	240
Thr	Tyr	Ser	Phe	Val	Ile	Lys	Arg	Leu	Pro	Leu	Phe	Tyr	Thr	Leu	Phe	245	250	255	
Leu	Ile	Ile	Pro	Cys	Ile	Gly	Leu	Ser	Phe	Leu	Thr	Val	Leu	Val	Phe	260	265	270	
Tyr	Leu	Pro	Ser	Asn	Glu	Gly	Glu	Lys	Ile	Cys	Leu	Cys	Thr	Ser	Val	275	280	285	
Leu	Val	Ser	Leu	Thr	Val	Phe	Leu	Leu	Val	Ile	Glu	Glu	Ile	Ile	Pro	290	295	300	
Ser	Ser	Ser	Lys	Val	Ile	Pro	Leu	Ile	Gly	Glu	Tyr	Leu	Val	Phe	Thr	305	310	315	320
Met	Ile	Phe	Val	Thr	Leu	Ser	Ile	Met	Val	Thr	Val	Phe	Ala	Ile	Asn				

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1743 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 143..1627
(D) OTHER INFORMATION: /product= "ALPHA-6 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGTTTTTGA	TTTCTGAGAA	GACACACACG	GATTGCAGTG	GGCTTCTGAT	GATGTCAAGG	60										
TTGGATGCAT	GTGGCTGACT	GATAGCTCTT	TGTTTTCCAC	AATCCTTTGC	CTAGGAAAAA	120										
GGAATCCAAG	TGTGTTTTAA	CC	ATG	CTG	ACC	AGC	AAG	GGG	CAG	GGA	TTC	CTT	172			
			Met	Leu	Thr	Ser	Lys	Gly	Gln	Gly	Phe	Leu				
			1				5					10				
CAT	GGG	GGC	TTG	TGT	CTC	TGG	CTG	TGT	GTG	TTC	ACA	CCT	TTC	TTT	AAA	220
His	Gly	Gly	Leu	Cys	Leu	Trp	Leu	Cys	Val	Phe	Thr	Pro	Phe	Phe	Lys	
				15					20					25		
GGC	TGT	GTG	GGC	TGT	GCA	ACT	GAG	GAG	AGG	CTC	TTC	CAC	AAA	CTG	TTT	268

Gly	Cys	Val	Gly 30	Cys	Ala	Thr	Glu	Glu 35	Arg	Leu	Phe	His	Lys 40	Leu	Phe		
TCT	CAT	TAC	AAC	CAG	TTC	ATC	AGG	CCT	GTG	GAA	AAC	GTT	TCC	GAC	CCT		316
Ser	His	Tyr 45	Asn	Gln	Phe	Ile	Arg 50	Pro	Val	Glu	Asn	Val 55	Ser	Asp	Pro		
GTC	ACG	GTA	CAC	TTT	GAA	GTG	GCC	ATC	ACC	CAG	CTG	GCC	AAC	GTG	GAT		364
Val	Thr 60	Val	His	Phe	Glu	Val 65	Ala	Ile	Thr	Gln	Leu 70	Ala	Asn	Val	Asp		
GAA	GTA	AAC	CAG	ATC	ATG	GAA	ACC	AAT	TTG	TGG	CTG	CGT	CAC	ATC	TGG		412
Glu 75	Val	Asn	Gln	Ile	Met 80	Glu	Thr	Asn	Leu	Trp 85	Leu	Arg	His	Ile	Trp 90		
AAT	GAT	TAT	AAA	TTG	CGC	TGG	GAT	CCA	ATG	GAA	TAT	GAT	GGC	ATT	GAG		460
Asn	Asp	Tyr	Lys	Leu 95	Arg	Trp	Asp	Pro	Met 100	Glu	Tyr	Asp	Gly	Ile 105	Glu		
ACT	CTT	CGC	GTT	CCT	GCA	GAT	AAG	ATT	TGG	AAG	CCC	GAC	ATT	GTT	CTC		508
Thr	Leu	Arg	Val 110	Pro	Ala	Asp	Lys	Ile 115	Trp	Lys	Pro	Asp	Ile 120	Val	Leu		
TAT	AAC	AAT	GCT	GTT	GGT	GAC	TTC	CAA	GTA	GAA	GGC	AAA	ACA	AAA	GCT		556
Tyr	Asn	Asn 125	Ala	Val	Gly	Asp	Phe 130	Gln	Val	Glu	Gly	Lys 135	Thr	Lys	Ala		
CTT	CTT	AAA	TAC	AAT	GGC	ATG	ATA	ACC	TGG	ACT	CCA	CCA	GCT	ATT	TTT		604
Leu 140	Leu	Lys	Tyr	Asn	Gly	Met 145	Ile	Thr	Trp	Thr	Pro 150	Pro	Ala	Ile	Phe		
AAG	AGT	TCC	TGC	CCT	ATG	GAT	ATC	ACC	TTT	TTC	CCT	TTT	GAT	CAT	CAA		652
Lys 155	Ser	Ser	Cys	Pro	Met 160	Asp	Ile	Thr	Phe	Phe 165	Pro	Phe	Asp	His	Gln 170		
AAC	TGT	TCC	CTA	AAA	TTT	GGT	TCC	TGG	ACG	TAT	GAC	AAA	GCT	GAA	ATT		700
Asn	Cys	Ser	Leu	Lys 175	Phe	Gly	Ser	Trp	Thr 180	Tyr	Asp	Lys	Ala	Glu 185	Ile		
GAT	CTT	CTA	ATC	ATT	GGA	TCA	AAA	GTG	GAT	ATG	AAT	GAT	TTT	TGG	GAA		748
Asp	Leu	Leu 190	Ile	Ile	Gly	Ser	Lys	Val 195	Asp	Met	Asn	Asp	Phe 200	Trp	Glu		
AAC	AGT	GAA	TGG	GAA	ATC	ATT	GAT	GCC	TCT	GGC	TAC	AAA	CAT	GAC	ATC		796
Asn	Ser	Glu 205	Trp	Glu	Ile	Ile	Asp 210	Ala	Ser	Gly	Tyr	Lys 215	His	Asp	Ile		
AAA	TAC	AAC	TGT	TGT	GAA	GAG	ATA	TAC	ACA	GAT	ATA	ACC	TAT	TCT	TTC		844
Lys 220	Tyr	Asn	Cys	Cys	Glu	Glu 225	Ile	Tyr	Thr	Asp	Ile 230	Thr	Tyr	Ser	Phe		
TAC	ATT	AGA	AGA	TTG	CCG	ATG	TTT	TAC	ACG	ATT	AAT	CTG	ATC	ATC	CCT		892
Tyr 235	Ile	Arg	Arg	Leu	Pro 240	Met	Phe	Tyr	Thr	Ile 245	Asn	Leu	Ile	Ile	Pro 250		
TGT	CTC	TTT	ATT	TCA	TTT	CTA	ACC	GTG	TTG	GTC	TTT	TAC	CTT	CCT	TCG		940
Cys	Leu	Phe	Ile	Ser 255	Phe	Leu	Thr	Val	Leu 260	Val	Phe	Tyr	Leu	Pro 265	Ser		
GAC	TGT	GGT	GAA	AAA	GTG	ACG	CTT	TGT	ATT	TCA	GTC	CTG	CTT	TCT	CTG		988
Asp	Cys	Gly	Glu 270	Lys	Val	Thr	Leu	Cys 275	Ile	Ser	Val	Leu	Leu 280	Ser	Leu		

ACT	GTG	TTT	TTG	CTG	GTC	ATC	ACA	GAA	ACC	ATC	CCA	TCC	ACA	TCT	CTG	1036
Thr	Val	Phe	Leu	Leu	Val	Ile	Thr	Glu	Thr	Ile	Pro	Ser	Thr	Ser	Leu	
		285					290					295				
GTG	GTC	CCA	CTG	GTG	GGT	GAG	TAC	CTG	CTG	TTC	ACC	ATG	ATC	TTT	GTC	1084
Val	Val	Pro	Leu	Val	Gly	Glu	Tyr	Leu	Leu	Phe	Thr	Met	Ile	Phe	Val	
	300					305					310					
ACA	CTG	TCC	ATC	GTG	GTG	ACT	GTG	TTT	GTG	TTG	AAC	ATA	CAC	TAC	CGC	1132
Thr	Leu	Ser	Ile	Val	Val	Thr	Val	Phe	Val	Leu	Asn	Ile	His	Tyr	Arg	
315				320					325						330	
ACC	CCA	ACC	ACG	CAC	ACA	ATG	CCC	AGG	TGG	GTG	AAG	ACA	GTT	TTC	CTG	1180
Thr	Pro	Thr	Thr	His	Thr	Met	Pro	Arg	Trp	Val	Lys	Thr	Val	Phe	Leu	
				335				340						345		
AAG	CTG	CTG	CCC	CAG	GTC	CTG	CTG	ATG	AGG	TGG	CCT	CTG	GAC	AAG	ACA	1228
Lys	Leu	Leu	Pro	Gln	Val	Leu	Leu	Met	Arg	Trp	Pro	Leu	Asp	Lys	Thr	
			350					355					360			
AGG	GGC	ACA	GGC	TCT	GAT	GCA	GTG	CCC	AGA	GGC	CTT	GCC	AGG	AGG	CCT	1276
Arg	Gly	Thr	Gly	Ser	Asp	Ala	Val	Pro	Arg	Gly	Leu	Ala	Arg	Arg	Pro	
	365					370						375				
GCC	AAA	GGC	AAG	CTT	GCA	AGC	CAT	GGG	GAA	CCC	AGA	CAT	CTT	AAA	GAA	1324
Ala	Lys	Gly	Lys	Leu	Ala	Ser	His	Gly	Glu	Pro	Arg	His	Leu	Lys	Glu	
	380					385					390					
TGC	TTC	CAT	TGT	CAC	AAA	TCA	AAT	GAG	CTT	GCC	ACA	AGC	AAG	AGA	AGA	1372
Cys	Phe	His	Cys	His	Lys	Ser	Asn	Glu	Leu	Ala	Thr	Ser	Lys	Arg	Arg	
395				400				405						410		
TTA	AGT	CAT	CAG	CCA	TTA	CAG	TGG	GTG	GTG	GAA	AAT	TCG	GAG	CAC	TCG	1420
Leu	Ser	His	Gln	Pro	Leu	Gln	Trp	Val	Val	Glu	Asn	Ser	Glu	His	Ser	
			415					420						425		
CCT	GAA	GTT	GAA	GAT	GTG	ATT	AAC	AGT	GTT	CAG	TTC	ATA	GCA	GAA	AAC	1468
Pro	Glu	Val	Glu	Asp	Val	Ile	Asn	Ser	Val	Gln	Phe	Ile	Ala	Glu	Asn	
			430				435						440			
ATG	AAG	AGC	CAC	AAT	GAA	ACC	AAG	GAG	GTA	GAA	GAT	GAC	TGG	AAA	TAC	1516
Met	Lys	Ser	His	Asn	Glu	Thr	Lys	Glu	Val	Glu	Asp	Asp	Trp	Lys	Tyr	
		445					450					455				
GTG	GCC	ATG	GTG	GTG	GAC	AGA	GTA	TTT	CTT	TGG	GTA	TTT	ATA	ATT	GTC	1564
Val	Ala	Met	Val	Val	Asp	Arg	Val	Phe	Leu	Trp	Val	Phe	Ile	Ile	Val	
	460				465						470					
TGT	GTA	TTT	GGA	ACT	GCA	GGG	CTA	TTT	CTA	CAG	CCA	CTA	CTT	GGG	AAC	1612
Cys	Val	Phe	Gly	Thr	Ala	Gly	Leu	Phe	Leu	Gln	Pro	Leu	Leu	Gly	Asn	
475				480						485				490		
ACA	GGA	AAA	TCT	TAAAATGTAT	TTTCTTTTAT	GTTCAGAAAT	TTACAGACAC									1664
Thr	Gly	Lys	Ser													
				495												
CATATTTGTT	CTGCATTCCC	TGCCACAAGG	AAAGGAAAGC	AAAGGCTTCC	CACCCAAGTC											1724
CCCCATCTGC	TAAAACCCG															1743


```

Thr Leu Cys Ile Ser Val Leu Leu Ser Leu Thr Val Phe Leu Leu Val
  275                                280                285

Ile Thr Glu Thr Ile Pro Ser Thr Ser Leu Val Val Pro Leu Val Gly
  290                                295                300

Glu Tyr Leu Leu Phe Thr Met Ile Phe Val Thr Leu Ser Ile Val Val
  305                                310                315                320

Thr Val Phe Val Leu Asn Ile His Tyr Arg Thr Pro Thr Thr His Thr
  325                                330                335

Met Pro Arg Trp Val Lys Thr Val Phe Leu Lys Leu Leu Pro Gln Val
  340                                345                350

Leu Leu Met Arg Trp Pro Leu Asp Lys Thr Arg Gly Thr Gly Ser Asp
  355                                360                365

Ala Val Pro Arg Gly Leu Ala Arg Arg Pro Ala Lys Gly Lys Leu Ala
  370                                375                380

Ser His Gly Glu Pro Arg His Leu Lys Glu Cys Phe His Cys His Lys
  385                                390                395                400

Ser Asn Glu Leu Ala Thr Ser Lys Arg Arg Leu Ser His Gln Pro Leu
  405                                410                415

Gln Trp Val Val Glu Asn Ser Glu His Ser Pro Glu Val Glu Asp Val
  420                                425                430

Ile Asn Ser Val Gln Phe Ile Ala Glu Asn Met Lys Ser His Asn Glu
  435                                440                445

Thr Lys Glu Val Glu Asp Asp Trp Lys Tyr Val Ala Met Val Val Asp
  450                                455                460

Arg Val Phe Leu Trp Val Phe Ile Ile Val Cys Val Phe Gly Thr Ala
  465                                470                475                480

Gly Leu Phe Leu Gln Pro Leu Leu Gly Asn Thr Gly Lys Ser
  485                                490

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 73..1581
- (D) OTHER INFORMATION: /product= "ALPHA-7 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGCAGGC	GCAGGCCCCG	GCGACAGCCG	AGACGTGGAG	CGCGCCGGCT	CGCTGCAGCT	60
CCGGGACTCA	ACATGCGCTG	CTCGCCGGGA	GGCGTCTGGC	TGGCGCTGGC	CGCGTCGCTC	120
CTGCACGTGT	CCCTGCAAGG	CGAGTTCCAG	AGGAAGCTTT	ACAAGGAGCT	GGTCAAGAAC	180
TACAATCCCT	TGGAGAGGCC	CGTGGCCAAT	GACTCGCAAC	CACTCACCGT	CTACTTCTCC	240
CTGAGCCTCC	TGCAGATCAT	GGACGTGGAT	GAGAAGAACC	AAGTTTAAAC	CACCAACATT	300
TGGCTGCAAA	TGTCTTGGAC	AGATCACTAT	TTACAGTGGA	ATGTGTCAGA	ATATCCAGGG	360
GTGAAGACTG	TTCGTTTCCC	AGATGGCCAG	ATTTGGAAC	CAGACATTCT	TCTCTATAAC	420
AGTGCTGATG	AGCGCTTTGA	CGCCACATTC	CACACTAACG	TGTTGGTGAA	TTCTTCTGGG	480
CATTGCCAGT	ACCTGCCTCC	AGGCATATTC	AAGAGTTCCT	GCTACATCGA	TGTACGCTGG	540
TTTCCCTTTG	ATGTGCAGCA	CTGCAAACTG	AAGTTTGGGT	CCTGGTCTTA	CGGAGGCTGG	600
TCCTTGGATC	TGCAGATGCA	GGAGGCAGAT	ATCAGTGGCT	ATATCCCCAA	TGGAGAATGG	660
GACCTAGTGG	GAATCCCCGG	CAAGAGGAGT	GAAAAGTTC	ATGAGTGCTG	CAAAGAGCCC	720
TACCCCGATG	TCACCTTAC	AGTGACCATG	CGCCGCAGGA	CGCTCTACTA	TGGCCTCAAC	780
CTGCTGATCC	CCTGTGTGCT	CATCTCCGCC	CTCGCCCTGC	TGGTGTTCCT	GCTTCCTGCA	840
GATTCCGGGG	AGAAGATTTT	CCTGGGGATA	ACAGTCTTAC	TCTCTCTTAC	CGTCTTCATG	900
CTGCTCGTGG	CTGAGATCAT	GCCCGCAACA	TCCGATTCGG	TACCATTGAT	AGCCCAGTAC	960
TTCGCCAGCA	CCATGATCAT	CGTGGGCCTC	TCGGTGGTGG	TGACGGTGAT	CGTGCTGCAG	1020
TACCACCACC	ACGACCCCGA	CGGGGGCAAG	ATGCCCAAGT	GGACCAGAGT	CATCCTTCTG	1080
AACTGGTGCG	CGTGGTTCCT	SCGAATGAAG	AGGCCCGGGG	AGGACAAGGT	GCGCCCGGCC	1140
TGCCAGCACA	AGCAGCGGCG	CTGCAGCCTG	GCCAGTGTGG	AGATGAGCGC	CGTGGCGCCG	1200
CCGCCCGCCA	GCAACGGGAA	CCTGCTGTAC	ATCGGCTTCC	GCGGCCTGGA	CGGCGTGCAC	1260
TGTGTCCCGA	CCCCCGACTC	TGGGGTAGTG	TGTGGCCGCA	TGGCCTGCTC	CCCCACGCAC	1320
GATGAGCACC	TCCTGCACGG	CGGGCAACCC	CCCGAGGGGG	ACCCGGACTT	GGCCAAGATC	1380
CTGGAGGAGG	TCCGCTACAT	TGCCAATCGC	TTCCGCTGCC	AGGACGAAAG	CGAGGCGGTC	1440
TGCAGCGAGT	GGAAGTTCGC	CGCCTGTGTG	GTGGACCGCC	TGTGCCTCAT	GGCCTTCTCG	1500
GTCTTCACCA	TCATCTGCAC	CATCGGCATC	CTGATGTCGG	CTCCCAACTT	CGTGGAGGCC	1560
GTGTCCAAAG	ACTTTGCGTA	ACCACGCCTG	GTTCTGTACA	TGTGGAAAAC	TCACAGATGG	1620
GCAAGGCCTT	TGGCTTGGCG	AGATTTGGGG	GTGCTAATCC	AGGACAGCAT	TACACGCCAC	1680
AACTCCAGTG	TTCCCTTCTG	GCTGTCAGTC	GTGTTGCTTA	CGGTTTCTTT	GTTACTTTAG	1740
GTAGTAGAAT	CTCAGCACTT	TGTTTCATAT	TCTCAGATGG	GCTGATAGAT	ATCCTTGGCA	1800
CATCCGTACC	ATCGGTCAGC	AGGGCCACTG	AGTAGTCATT	TTGCCCATTA	GCCCCTGACC	1860

TGGAAAGCCC TTCGGA

1876

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Arg	Cys	Ser	Pro	Gly	Gly	Val	Trp	Leu	Ala	Leu	Ala	Ala	Ser	Leu
1				5					10					15	
Leu	His	Val	Ser	Leu	Gln	Gly	Glu	Phe	Gln	Arg	Lys	Leu	Tyr	Lys	Glu
			20					25					30		
Leu	Val	Lys	Asn	Tyr	Asn	Pro	Leu	Glu	Arg	Pro	Val	Ala	Asn	Asp	Ser
		35					40					45			
Gln	Pro	Leu	Thr	Val	Tyr	Phe	Ser	Leu	Ser	Leu	Leu	Gln	Ile	Met	Asp
	50					55					60				
Val	Asp	Glu	Lys	Asn	Gln	Val	Leu	Thr	Thr	Asn	Ile	Trp	Leu	Gln	Met
65					70					75					80
Ser	Trp	Thr	Asp	His	Tyr	Leu	Gln	Trp	Asn	Val	Ser	Glu	Tyr	Pro	Gly
				85					90					95	
Val	Lys	Thr	Val	Arg	Phe	Pro	Asp	Gly	Gln	Ile	Trp	Lys	Pro	Asp	Ile
			100					105					110		
Leu	Leu	Tyr	Asn	Ser	Ala	Asp	Glu	Arg	Phe	Asp	Ala	Thr	Phe	His	Thr
		115					120					125			
Asn	Val	Leu	Val	Asn	Ser	Ser	Gly	His	Cys	Gln	Tyr	Leu	Pro	Pro	Gly
	130					135					140				
Ile	Phe	Lys	Ser	Ser	Cys	Tyr	Ile	Asp	Val	Arg	Trp	Phe	Pro	Phe	Asp
145					150				155						160
Val	Gln	His	Cys	Lys	Leu	Lys	Phe	Gly	Ser	Trp	Ser	Tyr	Gly	Gly	Trp
				165					170					175	
Ser	Leu	Asp	Leu	Gln	Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Tyr	Ile	Pro
			180					185					190		
Asn	Gly	Glu	Trp	Asp	Leu	Val	Gly	Ile	Pro	Gly	Lys	Arg	Ser	Glu	Arg
		195					200					205			
Phe	Tyr	Glu	Cys	Cys	Lys	Glu	Pro	Tyr	Pro	Asp	Val	Thr	Phe	Thr	Val
	210					215					220				
Thr	Met	Arg	Arg	Arg	Thr	Leu	Tyr	Tyr	Gly	Leu	Asn	Leu	Leu	Ile	Pro
225					230					235					240
Cys	Val	Leu	Ile	Ser	Ala	Leu	Ala	Leu	Leu	Val	Phe	Leu	Leu	Pro	Ala

245										250					255				
Asp	Ser	Gly	Glu	Lys	Ile	Ser	Leu	Gly	Ile	Thr	Val	Leu	Leu	Ser	Leu				
			260					265					270						
Thr	Val	Phe	Met	Leu	Leu	Val	Ala	Glu	Ile	Met	Pro	Ala	Thr	Ser	Asp				
		275					280					285							
Ser	Val	Pro	Leu	Ile	Ala	Gln	Tyr	Phe	Ala	Ser	Thr	Met	Ile	Ile	Val				
	290					295					300								
Gly	Leu	Ser	Val	Val	Val	Thr	Val	Ile	Val	Leu	Gln	Tyr	His	His	His				
305					310					315					320				
Asp	Pro	Asp	Gly	Gly	Lys	Met	Pro	Lys	Trp	Thr	Arg	Val	Ile	Leu	Leu				
				325					330					335					
Asn	Trp	Cys	Ala	Trp	Phe	Leu	Arg	Met	Lys	Arg	Pro	Gly	Glu	Asp	Lys				
			340					345					350						
Val	Arg	Pro	Ala	Cys	Gln	His	Lys	Gln	Arg	Arg	Cys	Ser	Leu	Ala	Ser				
		355					360					365							
Val	Glu	Met	Ser	Ala	Val	Ala	Pro	Pro	Pro	Ala	Ser	Asn	Gly	Asn	Leu				
	370					375					380								
Leu	Tyr	Ile	Gly	Phe	Arg	Gly	Leu	Asp	Gly	Val	His	Cys	Val	Pro	Thr				
385					390					395					400				
Pro	Asp	Ser	Gly	Val	Val	Cys	Gly	Arg	Met	Ala	Cys	Ser	Pro	Thr	His				
				405					410					415					
Asp	Glu	His	Leu	Leu	His	Gly	Gly	Gln	Pro	Pro	Glu	Gly	Asp	Pro	Asp				
			420					425					430						
Leu	Ala	Lys	Ile	Leu	Glu	Glu	Val	Arg	Tyr	Ile	Ala	Asn	Arg	Phe	Arg				
		435					440					445							
Cys	Gln	Asp	Glu	Ser	Glu	Ala	Val	Cys	Ser	Glu	Trp	Lys	Phe	Ala	Ala				
	450					455					460								
Cys	Val	Val	Asp	Arg	Leu	Cys	Leu	Met	Ala	Phe	Ser	Val	Phe	Thr	Ile				
465					470					475					480				
Ile	Cys	Thr	Ile	Gly	Ile	Leu	Met	Ser	Ala	Pro	Asn	Phe	Val	Glu	Ala				
				485					490					495					
Val	Ser	Lys	Asp	Phe	Ala														
				500															

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 265..1773

(D) OTHER INFORMATION: /product= "BETA-2 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCTCCCC TCACCGTCCC AATTGTATTC CCTGGAAGAG CAGCCGGAAG AGCCTCCGCC	60
TGCTCATACC AGGATAGGCA AGAAGCTGGT TTCTCCTCGC AGCCGGCTCC CTGAGGCCCA	120
GGAACCACCG CGGCGGCCGG CACCACCTGG ACCCAGCTCC AGGCGGGCGC GGCTTCAGCA	180
CCACGGACAG CGCCCCACCC GCGGCCCTCC CCCC GGCGGC GCGCTCCAGC CGGTGTAGGC	240
GAGGCAGCGA GCTATGCCCG CGGC ATG GCC CGG CGC TGC GGC CCC GTG GCG	291
Met Ala Arg Arg Cys Gly Pro Val Ala	
1 5	
CTG CTC CTT GGC TTC GGC CTC CTC CGG CTG TGC TCA GGG GTG TGG GGT	339
Leu Leu Leu Gly Phe Gly Leu Leu Arg Leu Cys Ser Gly Val Trp Gly	
10 15 20 25	
ACG GAT ACA GAG GAG CGG CTG GTG GAG CAT CTC CTG GAT CCT TCC CGC	387
Thr Asp Thr Glu Glu Arg Leu Val Glu His Leu Leu Asp Pro Ser Arg	
30 35 40	
TAC AAC AAG CTT ATC CGC CCA GCC ACC AAT GGC TCT GAG CTG GTG ACA	435
Tyr Asn Lys Leu Ile Arg Pro Ala Thr Asn Gly Ser Glu Leu Val Thr	
45 50 55	
GTA CAG CTT ATG GTG TCA CTG GCC CAG CTC ATC AGT GTG CAT GAG CGG	483
Val Gln Leu Met Val Ser Leu Ala Gln Leu Ile Ser Val His Glu Arg	
60 65 70	
GAG CAG ATC ATG ACC ACC AAT GTC TGG CTG ACC CAG GAG TGG GAA GAT	531
Glu Gln Ile Met Thr Thr Asn Val Trp Leu Thr Gln Glu Trp Glu Asp	
75 80 85	
TAT CGC CTC ACC TGG AAG CCT GAA GAG TTT GAC AAC ATG AAG AAA GTT	579
Tyr Arg Leu Thr Trp Lys Pro Glu Glu Phe Asp Asn Met Lys Lys Val	
90 95 100 105	
CGG CTC CCT TCC AAA CAC ATC TGG CTC CCA GAT GTG GTC CTG TAC AAC	627
Arg Leu Pro Ser Lys His Ile Trp Leu Pro Asp Val Val Leu Tyr Asn	
110 115 120	
AAT GCT GAC GGC ATG TAC GAG GTG TCC TTC TAT TCC AAT GCC GTG GTC	675
Asn Ala Asp Gly Met Tyr Glu Val Ser Phe Tyr Ser Asn Ala Val Val	
125 130 135	
TCC TAT GAT GGC AGC ATC TTC TGG CTG CCG CCT GCC ATC TAC AAG AGC	723
Ser Tyr Asp Gly Ser Ile Phe Trp Leu Pro Pro Ala Ile Tyr Lys Ser	
140 145 150	
GCA TGC AAG ATT GAA GTA AAG CAC TTC CCA TTT GAC CAG CAG AAC TGC	771
Ala Cys Lys Ile Glu Val Lys His Phe Pro Phe Asp Gln Gln Asn Cys	
155 160 165	
ACC ATG AAG TTC CGT TCG TGG ACC TAC GAC CGC ACA GAG ATC GAC TTG	819
Thr Met Lys Phe Arg Ser Trp Thr Tyr Asp Arg Thr Glu Ile Asp Leu	

170					175					180					185	
GTG	CTG	AAG	AGT	GAG	GTG	GCC	AGC	CTG	GAC	GAC	TTC	ACA	CCT	AGT	GGT	867
Val	Leu	Lys	Ser	Glu	Val	Ala	Ser	Leu	Asp	Asp	Phe	Thr	Pro	Ser	Gly	
				190					195					200		
GAG	TGG	GAC	ATC	GTG	GCG	CTG	CCG	GGC	CGG	CGC	AAC	GAG	AAC	CCC	GAC	915
Glu	Trp	Asp	Ile	Val	Ala	Leu	Pro	Gly	Arg	Arg	Asn	Glu	Asn	Pro	Asp	
			205					210					215			
GAC	TCT	ACG	TAC	GTG	GAC	ATC	ACG	TAT	GAC	TTC	ATC	ATT	CGC	CGC	AAG	963
Asp	Ser	Thr	Tyr	Val	Asp	Ile	Thr	Tyr	Asp	Phe	Ile	Ile	Arg	Arg	Lys	
			220				225					230				
CCG	CTC	TTC	TAC	ACC	ATC	AAC	CTC	ATC	ATC	CCC	TGT	GTG	CTC	ATC	ACC	1011
Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile	Ile	Pro	Cys	Val	Leu	Ile	Thr	
	235					240					245					
TCG	CTA	GCC	ATC	CTT	GTC	TTC	TAC	CTG	CCA	TCC	GAC	TGT	GGC	GAG	AAG	1059
Ser	Leu	Ala	Ile	Leu	Val	Phe	Tyr	Leu	Pro	Ser	Asp	Cys	Gly	Glu	Lys	
250					255					260					265	
ATG	ACG	TTG	TGC	ATC	TCA	GTG	CTG	CTG	GCG	CTC	ACG	GTC	TTC	CTG	CTG	1107
Met	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu	Ala	Leu	Thr	Val	Phe	Leu	Leu	
				270					275					280		
CTC	ATC	TCC	AAG	ATC	GTG	CCT	CCC	ACC	TCC	CTC	GAC	GTG	CCG	CTC	GTC	1155
Leu	Ile	Ser	Lys	Ile	Val	Pro	Pro	Thr	Ser	Leu	Asp	Val	Pro	Leu	Val	
			285					290					295			
GGC	AAG	TAC	CTC	ATG	TTC	ACC	ATG	GTG	CTT	GTC	ACC	TTC	TCC	ATC	GTC	1203
Gly	Lys	Tyr	Leu	Met	Phe	Thr	Met	Val	Leu	Val	Thr	Phe	Ser	Ile	Val	
		300					305					310				
ACC	AGC	GTG	TGC	GTG	CTC	AAC	GTG	CAC	CAC	CGC	TCG	CCC	ACC	ACG	CAC	1251
Thr	Ser	Val	Cys	Val	Leu	Asn	Val	His	His	Arg	Ser	Pro	Thr	Thr	His	
	315					320					325					
ACC	ATG	GCG	CCC	TGG	GTG	AAG	GTC	GTC	TTC	CTG	GAG	AAG	CTG	CCC	GCG	1299
Thr	Met	Ala	Pro	Trp	Val	Lys	Val	Val	Phe	Leu	Glu	Lys	Leu	Pro	Ala	
330					335					340					345	
CTG	CTC	TTC	ATG	CAG	CAG	CCA	CGC	CAT	CAT	TGC	GCC	CGT	CAG	CGC	CTG	1347
Leu	Leu	Phe	Met	Gln	Gln	Pro	Arg	His	His	Cys	Ala	Arg	Gln	Arg	Leu	
				350					355					360		
CGC	CTG	CGG	CGA	CGC	CAG	CGT	GAG	CGC	GAG	GGC	GCT	GGA	GCC	CTC	TTC	1395
Arg	Leu	Arg	Arg	Arg	Gln	Arg	Glu	Arg	Glu	Gly	Ala	Gly	Ala	Leu	Phe	
			365					370					375			
TTC	CGC	GAA	GCC	CCA	GGG	GCC	GAC	TCC	TGC	ACG	TGC	TTC	GTC	AAC	CGC	1443
Phe	Arg	Glu	Ala	Pro	Gly	Ala	Asp	Ser	Cys	Thr	Cys	Phe	Val	Asn	Arg	
		380					385					390				
GCG	TCG	GTG	CAG	GGG	TTG	GCC	GGG	GCC	TTC	GGG	GCT	GAG	CCT	GCA	CCA	1491
Ala	Ser	Val	Gln	Gly	Leu	Ala	Gly	Ala	Phe	Gly	Ala	Glu	Pro	Ala	Pro	
	395					400					405					
GTG	GCG	GGC	CCC	GGG	CGC	TCA	GGG	GAG	CCG	TGT	GGC	TGT	GGC	CTC	CGG	1539
Val	Ala	Gly	Pro	Gly	Arg	Ser	Gly	Glu	Pro	Cys	Gly	Cys	Gly	Leu	Arg	
410					415					420					425	

GAG GCG GTG GAC GGC GTG CGC TTC ATC GCA GAC CAC ATG CGG AGC GAG	1587
Glu Ala Val Asp Gly Val Arg Phe Ile Ala Asp His Met Arg Ser Glu	
430 435 440	
GAC GAT GAC CAG AGC GTG AGT GAG GAC TGG AAG TAC GTC GCC ATG GTG	1635
Asp Asp Asp Gln Ser Val Ser Glu Asp Trp Lys Tyr Val Ala Met Val	
445 450 455	
ATC GAC CGC CTC TTC CTC TGG ATC TTT GTC TTT GTC TGT GTC TTT GGC	1683
Ile Asp Arg Leu Phe Leu Trp Ile Phe Val Phe Val Cys Val Phe Gly	
460 465 470	
ACC ATC GGC ATG TTC CTG CAG CCT CTC TTC CAG AAC TAC ACC ACC ACC	1731
Thr Ile Gly Met Phe Leu Gln Pro Leu Phe Gln Asn Tyr Thr Thr Thr	
475 480 485	
ACC TTC CTC CAC TCA GAC CAC TCA GCC CCC AGC TCC AAG TGAGGCCCTT	1780
Thr Phe Leu His Ser Asp His Ser Ala Pro Ser Ser Lys	
490 495 500	
CCTCATCTCC ATGCTCTTTC ACCCTGCCAC CCTCTGCTGC ACAGTAGTGT TGGGTGGAGG	1840
ATGGACGAGT GAGCTACCAG GAAGAGGGGC GCTGCCCCCA CAGATCCATC CTTTTGCTTC	1900
ATCTGGAGTC CCTCCTCCCC CACGCCTCCA TCCACACACA GCAGCTCCAA CCTGGAGGCT	1960
GGACCAACTG CTTTGTTTTG GCTGCTCTCC ATCTCTTGTA CCAGCCCAGG CAATAGTGTT	2020
GAGGAGGGGA GCAAGGCTGC TAAGTGAAG ACAGAGATGG CAGAGCCATC CACCCTGAGG	2080
AGTGACGGGC AAGGGGCCAG GAAGGGGACA GGATTGTCTG CTGCCTCCAA GTCATGGGAG	2140
AAGAGGGGTA TAGGACAAGG GGTGGAAGGG CAGGAGCTCA CACCGCACCG GGCTGGCCTG	2200
ACACAATGGT AGCTCTGAAG GGAGGGGAAG AGAGAGGCCT GGGTGTGACC TGACACCTGC	2260
CGCTGCTTGA GTGGACAGCA GCTGGACTGG GTGGGCCCCA CAGTGGTCAG CGATTCTGTC	2320
CAAGTAGGGT TTAGCCGGGC CCCATGGTCA CAGACCCCTG GGGGAGGCTT CCAGCTCAGT	2380
CCCACAGCCC CTTGCTTCTA AGGGATCCAG AGACCTGCTC CAGATCCTCT TTCCCCACTG	2440
AAGAATTC	2448

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Arg	Arg	Cys	Gly	Pro	Val	Ala	Leu	Leu	Leu	Gly	Phe	Gly	Leu
1				5					10					15	
Leu	Arg	Leu	Cys	Ser	Gly	Val	Trp	Gly	Thr	Asp	Thr	Glu	Glu	Arg	Leu
			20					25					30		

Val Glu His Leu Leu Asp Pro Ser Arg Tyr Asn Lys Leu Ile Arg Pro
 35 40 45
 Ala Thr Asn Gly Ser Glu Leu Val Thr Val Gln Leu Met Val Ser Leu
 50 55 60
 Ala Gln Leu Ile Ser Val His Glu Arg Glu Gln Ile Met Thr Thr Asn
 65 70 75 80
 Val Trp Leu Thr Gln Glu Trp Glu Asp Tyr Arg Leu Thr Trp Lys Pro
 85 90 95
 Glu Glu Phe Asp Asn Met Lys Lys Val Arg Leu Pro Ser Lys His Ile
 100 105 110
 Trp Leu Pro Asp Val Val Leu Tyr Asn Asn Ala Asp Gly Met Tyr Glu
 115 120 125
 Val Ser Phe Tyr Ser Asn Ala Val Val Ser Tyr Asp Gly Ser Ile Phe
 130 135 140
 Trp Leu Pro Pro Ala Ile Tyr Lys Ser Ala Cys Lys Ile Glu Val Lys
 145 150 155 160
 His Phe Pro Phe Asp Gln Gln Asn Cys Thr Met Lys Phe Arg Ser Trp
 165 170 175
 Thr Tyr Asp Arg Thr Glu Ile Asp Leu Val Leu Lys Ser Glu Val Ala
 180 185 190
 Ser Leu Asp Asp Phe Thr Pro Ser Gly Glu Trp Asp Ile Val Ala Leu
 195 200 205
 Pro Gly Arg Arg Asn Glu Asn Pro Asp Asp Ser Thr Tyr Val Asp Ile
 210 215 220
 Thr Tyr Asp Phe Ile Ile Arg Arg Lys Pro Leu Phe Tyr Thr Ile Asn
 225 230 235 240
 Leu Ile Ile Pro Cys Val Leu Ile Thr Ser Leu Ala Ile Leu Val Phe
 245 250 255
 Tyr Leu Pro Ser Asp Cys Gly Glu Lys Met Thr Leu Cys Ile Ser Val
 260 265 270
 Leu Leu Ala Leu Thr Val Phe Leu Leu Leu Ile Ser Lys Ile Val Pro
 275 280 285
 Pro Thr Ser Leu Asp Val Pro Leu Val Gly Lys Tyr Leu Met Phe Thr
 290 295 300
 Met Val Leu Val Thr Phe Ser Ile Val Thr Ser Val Cys Val Leu Asn
 305 310 315 320
 Val His His Arg Ser Pro Thr Thr His Thr Met Ala Pro Trp Val Lys
 325 330 335
 Val Val Phe Leu Glu Lys Leu Pro Ala Leu Leu Phe Met Gln Gln Pro
 340 345 350
 Arg His His Cys Ala Arg Gln Arg Leu Arg Leu Arg Arg Arg Gln Arg

355	360	365
Glu Arg Glu Gly Ala Gly Ala Leu Phe Phe Arg Glu Ala Pro Gly Ala		
370	375	380
Asp Ser Cys Thr Cys Phe Val Asn Arg Ala Ser Val Gln Gly Leu Ala		
385	390	395
Gly Ala Phe Gly Ala Glu Pro Ala Pro Val Ala Gly Pro Gly Arg Ser		
	405	410
Gly Glu Pro Cys Gly Cys Gly Leu Arg Glu Ala Val Asp Gly Val Arg		
	420	425
Phe Ile Ala Asp His Met Arg Ser Glu Asp Asp Asp Gln Ser Val Ser		
	435	440
Glu Asp Trp Lys Tyr Val Ala Met Val Ile Asp Arg Leu Phe Leu Trp		
	450	455
Ile Phe Val Phe Val Cys Val Phe Gly Thr Ile Gly Met Phe Leu Gln		
465	470	475
Pro Leu Phe Gln Asn Tyr Thr Thr Thr Thr Phe Leu His Ser Asp His		
	485	490
Ser Ala Pro Ser Ser Lys		
	500	

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 98..1474
- (D) OTHER INFORMATION: /product= "BETA-3 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGGAACCCC TGTATTTTCT TTTCAAAACC CCCTTTTCCA GTGGAAATGC TCTGTTGTTA	60
AAAAGGAAGA AACTGTCTTT CTGAAACTGA CATCACG ATG CTC CCA GAT TTT ATG	115
Met Leu Pro Asp Phe Met	5
1	
CTG GTT CTC ATC GTC CTT GGC ATC CCT TCC TCA GCC ACC ACA GGT TTC	163
Leu Val Leu Ile Val Leu Gly Ile Pro Ser Ser Ala Thr Thr Gly Phe	
10	15
20	
AAC TCA ATC GCC GAA AAT GAA GAT GCC CTC CTC AGA CAT TTG TTC CAA	211
Asn Ser Ile Ala Glu Asn Glu Asp Ala Leu Leu Arg His Leu Phe Gln	
25	30
35	

GGT Gly	TAT Tyr	CAG Gln	AAA Lys	TGG Trp	GTC Val	CGC Arg	CCT Pro	GTA Val	TTA Leu	CAT His	TCT Ser	AAT Asn	GAC Asp	ACC Thr	ATA Ile	259
	40					45					50					
AAA Lys	GTA Val	TAT Tyr	TTT Phe	GGA Gly	TTG Leu	AAA Lys	ATA Ile	TCC Ser	CAG Gln	CTT Leu	GTA Val	GAT Asp	GTG Val	GAT Asp	GAA Glu	307
	55				60					65					70	
AAG Lys	AAT Asn	CAG Gln	CTG Leu	ATG Met	ACA Thr	ACC Thr	AAT Asn	GTG Val	TGG Trp	CTC Leu	AAA Lys	CAG Gln	GAA Glu	TGG Trp	ACA Thr	355
				75					80					85		
GAC Asp	CAC His	AAG Lys	TTA Leu	CGC Arg	TGG Trp	AAT Asn	CCT Pro	GAT Asp	GAT Asp	TAT Tyr	GGT Gly	GGG Gly	ATC Ile	CAT His	TCC Ser	403
			90					95					100			
ATT Ile	AAA Lys	GTT Val	CCA Pro	TCA Ser	GAA Glu	TCT Ser	CTG Leu	TGG Trp	CTT Leu	CCT Pro	GAC Asp	ATA Ile	GTT Val	CTC Leu	TTT Phe	451
		105					110					115				
GAA Glu	AAT Asn	GCT Ala	GAC Asp	GGC Gly	CGC Arg	TTC Phe	GAA Glu	GGC Gly	TCC Ser	CTG Leu	ATG Met	ACC Thr	AAG Lys	GTC Val	ATC Ile	499
	120					125					130					
GTG Val	AAA Lys	TCA Ser	AAC Asn	GGA Gly	ACT Thr	GTT Val	GTC Val	TGG Trp	ACC Thr	CCT Pro	CCC Pro	GCC Ala	AGC Ser	TAC Tyr	AAA Lys	547
	135				140					145					150	
AGC Ser	TCC Ser	TGC Cys	ACC Thr	ATG Met	GAC Asp	GTC Val	ACG Thr	TTT Phe	TTC Phe	CCG Pro	TTC Phe	GAC Asp	CGA Arg	CAG Gln	AAC Asn	595
				155					160					165		
TGC Cys	TCC Ser	ATG Met	AAG Lys	TTT Phe	GGA Gly	TCC Ser	TGG Trp	ACT Thr	TAT Tyr	GAT Asp	GGC Gly	ACC Thr	ATG Met	GTT Val	GAC Asp	643
			170					175					180			
CTC Leu	ATT Ile	TTG Leu	ATC Ile	AAT Asn	GAA Glu	AAT Asn	GTC Val	GAC Asp	AGA Arg	AAA Lys	GAC Asp	TTC Phe	TTC Phe	GAT Asp	AAC Asn	691
		185					190					195				
GGA Gly	GAA Glu	TGG Trp	GAA Glu	ATA Ile	CTG Leu	AAT Asn	GCA Ala	AAG Lys	GGG Gly	ATG Met	AAG Lys	GGG Gly	AAC Asn	AGA Arg	AGG Arg	739
	200					205					210					
GAC Asp	GGC Gly	GTG Val	TAC Tyr	TCC Ser	TAT Tyr	CCC Pro	TTT Phe	ATC Ile	ACG Thr	TAT Tyr	TCC Ser	TTC Phe	GTC Val	CTG Leu	AGA Arg	787
	215				220					225					230	
CGC Arg	CTG Leu	CCT Pro	TTA Leu	TTC Phe	TAT Tyr	ACC Thr	CTC Leu	TTT Phe	CTC Leu	ATC Ile	ATC Ile	CCC Pro	TGC Cys	CTG Leu	GGG Gly	835
				235					240					245		
CTG Leu	TCT Ser	TTC Phe	CTA Leu	ACA Thr	GTT Val	CTT Leu	GTG Val	TTC Phe	TAT Tyr	TTA Leu	CCT Pro	TCG Ser	GAT Asp	GAA Glu	GGA Gly	883
			250					255					260			
GAA Glu	AAA Lys	CTT Leu	TCA Ser	TTA Leu	TCC Ser	ACA Thr	TCG Ser	GTC Val	TTG Leu	GTT Val	TCT Ser	CTG Leu	ACA Thr	GTT Val	TTC Phe	931
		265					270					275				
CTT Leu	TTA Leu	GTG Val	ATT Leu	GAA Glu	GAA Glu	ATC Leu	ATC Leu	CCA Pro	TCG Val	TCT Val	TCC Ser	AAA Lys	GTC Val	ATT Leu	CCT Leu	979

Leu	Leu	Val	Ile	Glu	Glu	Ile	Ile	Pro	Ser	Ser	Ser	Lys	Val	Ile	Pro																			
	280					285						290																						
CTC	ATT	GGA	GAG	TAC	CTG	CTG	TTC	ATC	ATG	ATT	TTT	GTG	ACC	CTG	TCC	1027																		
Leu	Ile	Gly	Glu	Tyr	Leu	Leu	Phe	Ile	Met	Ile	Phe	Val	Thr	Leu	Ser																			
295					300					305					310																			
ATC	ATT	GTT	ACC	GTG	TTT	GTC	ATT	AAC	GTT	CAC	CAC	AGA	TCT	TCT	TCC	1075																		
Ile	Ile	Val	Thr	Val	Phe	Val	Ile	Asn	Val	His	His	Arg	Ser	Ser	Ser																			
				315					320					325																				
ACG	TAC	CAC	CCC	ATG	GCC	CCC	TGG	GTT	AAG	AGG	CTC	TTT	CTG	CAG	AAA	1123																		
Thr	Tyr	His	Pro	Met	Ala	Pro	Trp	Val	Lys	Arg	Leu	Phe	Leu	Gln	Lys																			
			330					335					340																					
CTT	CCA	AAA	TTA	CTT	TGC	ATG	AAA	GAT	CAT	GTG	GAT	CGC	TAC	TCA	TCC	1171																		
Leu	Pro	Lys	Leu	Leu	Cys	Met	Lys	Asp	His	Val	Asp	Arg	Tyr	Ser	Ser																			
		345					350					355																						
CCA	GAG	AAA	GAG	GAG	AGT	CAA	CCA	GTA	GTG	AAA	GGC	AAA	GTC	CTC	GAA	1219																		
Pro	Glu	Lys	Glu	Glu	Ser	Gln	Pro	Val	Val	Lys	Gly	Lys	Val	Leu	Glu																			
	360					365					370																							
AAA	AAG	AAA	CAG	AAA	CAG	CTT	AGT	GAT	GGA	GAA	AAA	GTT	CTA	GTT	GCT	1267																		
Lys	Lys	Lys	Gln	Lys	Gln	Leu	Ser	Asp	Gly	Glu	Lys	Val	Leu	Val	Ala																			
375					380					385					390																			
TTT	TTG	GAA	AAA	GCT	GCT	GAT	TCC	ATT	AGA	TAC	ATT	TCC	AGA	CAT	GTG	1315																		
Phe	Leu	Glu	Lys	Ala	Ala	Asp	Ser	Ile	Arg	Tyr	Ile	Ser	Arg	His	Val																			
				395					400					405																				
AAG	AAA	GAA	CAT	TTT	ATC	AGC	CAG	GTA	GTA	CAA	GAC	TGG	AAA	TTT	GTA	1363																		
Lys	Lys	Glu	His	Phe	Ile	Ser	Gln	Val	Val	Gln	Asp	Trp	Lys	Phe	Val																			
			410					415					420																					
GCT	CAA	GTT	CTT	GAC	CGA	ATC	TTC	CTG	TGG	CTC	TTT	CTG	ATA	GTG	TCA	1411																		
Ala	Gln	Val	Leu	Asp	Arg	Ile	Phe	Leu	Trp	Leu	Phe	Leu	Ile	Val	Ser																			
		425					430					435																						
GCA	ACA	GGC	TCG	GTT	CTG	ATT	TTT	ACC	CCT	GCT	TTG	AAG	ATG	TGG	CTA	1459																		
Ala	Thr	Gly	Ser	Val	Leu	Ile	Phe	Thr	Pro	Ala	Leu	Lys	Met	Trp	Leu																			
	440					445					450																							
CAT	AGT	TAC	CAT	TAGGAATTTT							AAAAGACATA			AGTACTAAAT		TACACCTTAG	1511																	
His	Ser	Tyr	His																															
455																																		
ACCTGACATC TGGCTATCAC ACAGACAGAA TCCAAATGCA TGTGCTTGTT CTACGAACCC																1571																		
CGAATGCGTT GTCTTTGTGG AAATGGAACA TCTCCTCATG GGAGAAACTC TGGTAAATGT																1631																		
GCTCATTTGT GGTGCCATG AGAGTGAGCT GCTTTTAAAG AAAGTGAGC CTCCTCAGAC																1691																		
CCCTGCCTTG GCTTTCCCAG ACATTCAGGG AGGGATCATA GGTCCAGGCT TGAGCTCACA																1751																		
TGTGGCCAGA GTGCACAAA AGCTGTTGCT ACTTGGTGGA GGAACACCTC CTAGAAGCAG																1811																		
CAGGCCCTCG TGGTGGGGGA GGGGGGATTC ACCTGGAATT AAGGAAGTCT CGGTGTCGAG																1871																		
CTATCTGTGT GGGCAGAGCC TGGATCTCCC ACCCTGCACT GGCCTCCTTG GTGCCG																1927																		

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Met  Leu  Pro  Asp  Phe  Met  Leu  Val  Leu  Ile  Val  Leu  Gly  Ile  Pro  Ser
 1      5      10      15
Ser  Ala  Thr  Thr  Gly  Phe  Asn  Ser  Ile  Ala  Glu  Asn  Glu  Asp  Ala  Leu
      20      25      30
Leu  Arg  His  Leu  Phe  Gln  Gly  Tyr  Gln  Lys  Trp  Val  Arg  Pro  Val  Leu
      35      40      45
His  Ser  Asn  Asp  Thr  Ile  Lys  Val  Tyr  Phe  Gly  Leu  Lys  Ile  Ser  Gln
      50      55      60
Leu  Val  Asp  Val  Asp  Glu  Lys  Asn  Gln  Leu  Met  Thr  Thr  Asn  Val  Trp
      65      70      75      80
Leu  Lys  Gln  Glu  Trp  Thr  Asp  His  Lys  Leu  Arg  Trp  Asn  Pro  Asp  Asp
      85      90      95
Tyr  Gly  Gly  Ile  His  Ser  Ile  Lys  Val  Pro  Ser  Glu  Ser  Leu  Trp  Leu
      100     105     110
Pro  Asp  Ile  Val  Leu  Phe  Glu  Asn  Ala  Asp  Gly  Arg  Phe  Glu  Gly  Ser
      115     120     125
Leu  Met  Thr  Lys  Val  Ile  Val  Lys  Ser  Asn  Gly  Thr  Val  Val  Trp  Thr
      130     135     140
Pro  Pro  Ala  Ser  Tyr  Lys  Ser  Ser  Cys  Thr  Met  Asp  Val  Thr  Phe  Phe
      145     150     155     160
Pro  Phe  Asp  Arg  Gln  Asn  Cys  Ser  Met  Lys  Phe  Gly  Ser  Trp  Thr  Tyr
      165     170     175
Asp  Gly  Thr  Met  Val  Asp  Leu  Ile  Leu  Ile  Asn  Glu  Asn  Val  Asp  Arg
      180     185     190
Lys  Asp  Phe  Phe  Asp  Asn  Gly  Glu  Trp  Glu  Ile  Leu  Asn  Ala  Lys  Gly
      195     200     205
Met  Lys  Gly  Asn  Arg  Arg  Asp  Gly  Val  Tyr  Ser  Tyr  Pro  Phe  Ile  Thr
      210     215     220
Tyr  Ser  Phe  Val  Leu  Arg  Arg  Leu  Pro  Leu  Phe  Tyr  Thr  Leu  Phe  Leu
      225     230     235     240
Ile  Ile  Pro  Cys  Leu  Gly  Leu  Ser  Phe  Leu  Thr  Val  Leu  Val  Phe  Tyr
      245     250     255
Leu  Pro  Ser  Asp  Glu  Gly  Glu  Lys  Leu  Ser  Leu  Ser  Thr  Ser  Val  Leu
      260     265     270

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Val Ser Leu Thr Val Phe Leu Leu Val Ile Glu Glu Ile Ile Pro Ser
 275 280 285

Ser Ser Lys Val Ile Pro Leu Ile Gly Glu Tyr Leu Leu Phe Ile Met
 290 295 300

Ile Phe Val Thr Leu Ser Ile Ile Val Thr Val Phe Val Ile Asn Val
 305 310 315 320

His His Arg Ser Ser Ser Thr Tyr His Pro Met Ala Pro Trp Val Lys
 325 330 335

Arg Leu Phe Leu Gln Lys Leu Pro Lys Leu Leu Cys Met Lys Asp His
 340 345 350

Val Asp Arg Tyr Ser Ser Pro Glu Lys Glu Glu Ser Gln Pro Val Val
 355 360 365

Lys Gly Lys Val Leu Glu Lys Lys Lys Gln Lys Gln Leu Ser Asp Gly
 370 375 380

Glu Lys Val Leu Val Ala Phe Leu Glu Lys Ala Ala Asp Ser Ile Arg
 385 390 395 400

Tyr Ile Ser Arg His Val Lys Lys Glu His Phe Ile Ser Gln Val Val
 405 410 415

Gln Asp Trp Lys Phe Val Ala Gln Val Leu Asp Arg Ile Phe Leu Trp
 420 425 430

Leu Phe Leu Ile Val Ser Ala Thr Gly Ser Val Leu Ile Phe Thr Pro
 435 440 445

Ala Leu Lys Met Trp Leu His Ser Tyr His
 450 455

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 87..1583
- (D) OTHER INFORMATION: /product= "BETA-4 SUBUNIT"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCGGCGCTCA CTCGACCGCG CGGCTCACGG GTGCCCTGTG ACCCCACAGC GGAGCTCGCG	60
GCGGCTGCCA CCCGGCCCCG CCGGCCATGA GCGCGCGGCC TTCCCTGGTC CTTTCTTCC	120
TGGTCGCCCT TTGCGGGCGC GGGAAGTACC GCGTGGCCAA TCGGAGGAA AAGCTGATGG	180

ACGACCTTCT	GAACAAAACC	CGTTACAATA	ACCTGATCCG	CCCAGCCACC	AGCTCCTCAC	240
AGCTCATCTC	CATCAAGCTG	CAGCTCTCCC	TGGCCCAGCT	TATCAGCGTG	AATGAGCGAG	300
AGCAGATCAT	GACCACCAAT	GTCTGGCTGA	AACAGGAATG	GACTGATTAC	CGCCTGACCT	360
GGAACAGCTC	CCGCTACGAG	GGTGTGAACA	TCCTGAGGAT	CCCTGCAAAG	CGCATCTGGT	420
TGCCTGACAT	CGTGCTTTAC	AACAACGCCG	ACGGGACCTA	TGAGGTGTCT	GTCTACACCA	480
ACTTGATAGT	CCGGTCCAAC	GGCAGCGTCC	TGTGGCTGCC	CCCTGCCATC	TACAAGAGCG	540
CCTGCAAGAT	TGAGGTGAAG	TACTTTCCCT	TCGACCAGCA	GAAC TGACACC	CTCAAGTTCC	600
GCTCCTGGAC	CTATGACCAC	ACGGAGATAG	ACATGGTCCT	CATGACGCCC	ACAGCCAGCA	660
TGGATGACTT	TACTCCCAGT	GGTGAGTGGG	ACATAGTGGC	CCTCCCAGGG	AGAAGGACAG	720
TGAACCCACA	AGACCCAGC	TACGTGGACG	TGACTTACGA	CTTCATCATC	AAGCGCAAGC	780
CTCTGTTCTA	CACCATCAAC	CTCATCATCC	CCTGCGTGCT	CACCACCTTG	CTGGCCATCC	840
TCGTCTTCTA	CCTGCCATCC	GACTGCGGCG	AGAAGATGAC	ACTGTGCATC	TCAGTGCTGC	900
TGGCACTGAC	ATTCTTCCTG	CTGCTCATCT	CCAAGATCGT	GCCACCCACC	TCCCTCGATG	960
TGCCTCTCAT	CGGCAAGTAC	CTCATGTTCA	CCATGGTGCT	GGTCACCTTC	TCCATCGTCA	1020
CCAGCGTCTG	TGTGCTCAAT	GTGCACCACC	GCTCGCCCAG	CACCCACACC	ATGGCACCCCT	1080
GGGTCAAGCG	CTGCTTCCTG	CACAAGCTGC	CTACCTTCCT	CTTCATGAAG	CGCCCTGGCC	1140
CCGACAGCAG	CCCGGCCAGA	GCCTTCCCGC	CCAGCAAGTC	ATGCGTGACC	AAGCCCGAGG	1200
CCACCGCCAC	CTCCACCAGC	CCCTCCAAC	TCTATGGGAA	CTCCATGTAC	TTTGTGAACC	1260
CCGCCTCTGC	AGCTTCCAAG	TCTCCAGCCG	GCTCTACCCC	GGTGGCTATC	CCCAGGGATT	1320
TCTGGCTGCG	GTCCTCTGGG	AGGTTCCGAC	AGGATGTGCA	GGAGGCATTA	GAAGGTGTCA	1380
GCTTCATCGC	CCAGCACATG	AAGAATGACG	ATGAAGACCA	GAGTGTGCTT	GAGGACTGGA	1440
AGTACGTGGC	TATGGTGGTG	GACCGGCTGT	TCCTGTGGGT	GTTCATGTTT	GTGTGCGTCC	1500
TGGGCACTGT	GGGGCTCTTC	CTGCCGCCCC	TCTTCCAGAC	CCATGCAGCT	TCTGAGGGGC	1560
CCTACGCTGC	CCAGCGTGAC	TGAGGGCCCC	CTGGGTGTGT	GGGTGAGAGG	ATGTGAGTGG	1620
CCGGGTGGGC	ACTTTGCTGC	TTCTTTCTGG	GTTGTGGCCG	ATGAGGCCCT	AAGTAAATAT	1680
GTGAGCATTG	GCCATCAACC	CCATCAAACC	AGCCACAGCC	GTGGAACAGG	CAAGGATGGG	1740
GGCCTGGCCT	GTCCTCTCTG	AATGCCTTGG	AGGGATCCCA	GGAAGCCCCA	GTAGGAGGGA	1800
GCTTCAGACA	GTTCAATTCT	GGCCTGTCTT	CCTTCCCTGC	ACCGGGCAAT	GGGGATAAAG	1860
ATGACTTCGT	AGCAGCACCT	ACTATGCTTC	AGGCATGGTG	CCGGCCTGCC	TCTCC	1915

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met	Arg	Arg	Ala	Pro	Ser	Leu	Val	Leu	Phe	Phe	Leu	Val	Ala	Leu	Cys
1				5					10					15	
Gly	Arg	Gly	Asn	Cys	Arg	Val	Ala	Asn	Ala	Glu	Glu	Lys	Leu	Met	Asp
			20					25					30		
Asp	Leu	Leu	Asn	Lys	Thr	Arg	Tyr	Asn	Asn	Leu	Ile	Arg	Pro	Ala	Thr
		35					40					45			
Ser	Ser	Ser	Gln	Leu	Ile	Ser	Ile	Lys	Leu	Gln	Leu	Ser	Leu	Ala	Gln
	50					55					60				
Leu	Ile	Ser	Val	Asn	Glu	Arg	Glu	Gln	Ile	Met	Thr	Thr	Asn	Val	Trp
65					70					75					80
Leu	Lys	Gln	Glu	Trp	Thr	Asp	Tyr	Arg	Leu	Thr	Trp	Asn	Ser	Ser	Arg
				85					90				95		
Tyr	Glu	Gly	Val	Asn	Ile	Leu	Arg	Ile	Pro	Ala	Lys	Arg	Ile	Trp	Leu
			100					105					110		
Pro	Asp	Ile	Val	Leu	Tyr	Asn	Asn	Ala	Asp	Gly	Thr	Tyr	Glu	Val	Ser
		115					120					125			
Val	Tyr	Thr	Asn	Leu	Ile	Val	Arg	Ser	Asn	Gly	Ser	Val	Leu	Trp	Leu
	130					135					140				
Pro	Pro	Ala	Ile	Tyr	Lys	Ser	Ala	Cys	Lys	Ile	Glu	Val	Lys	Tyr	Phe
145					150					155					160
Pro	Phe	Asp	Gln	Gln	Asn	Cys	Thr	Leu	Lys	Phe	Arg	Ser	Trp	Thr	Tyr
				165					170					175	
Asp	His	Thr	Glu	Ile	Asp	Met	Val	Leu	Met	Thr	Pro	Thr	Ala	Ser	Met
			180					185					190		
Asp	Asp	Phe	Thr	Pro	Ser	Gly	Glu	Trp	Asp	Ile	Val	Ala	Leu	Pro	Gly
		195					200					205			
Arg	Arg	Thr	Val	Asn	Pro	Gln	Asp	Pro	Ser	Tyr	Val	Asp	Val	Thr	Tyr
		210				215					220				
Asp	Phe	Ile	Ile	Lys	Arg	Lys	Pro	Leu	Phe	Tyr	Thr	Ile	Asn	Leu	Ile
225					230					235					240
Ile	Pro	Cys	Val	Leu	Thr	Thr	Leu	Leu	Ala	Ile	Leu	Val	Phe	Tyr	Leu
				245					250					255	
Pro	Ser	Asp	Cys	Gly	Glu	Lys	Met	Thr	Leu	Cys	Ile	Ser	Val	Leu	Leu
			260					265					270		
Ala	Leu	Thr	Phe	Phe	Leu	Leu	Leu	Ile	Ser	Lys	Ile	Val	Pro	Pro	Thr

275					280					285					
Ser	Leu	Asp	Val	Pro	Leu	Ile	Gly	Lys	Tyr	Leu	Met	Phe	Thr	Met	Val
290					295					300					
Leu	Val	Thr	Phe	Ser	Ile	Val	Thr	Ser	Val	Cys	Val	Leu	Asn	Val	His
305					310					315					320
His	Arg	Ser	Pro	Ser	Thr	His	Thr	Met	Ala	Pro	Trp	Val	Lys	Arg	Cys
				325					330					335	
Phe	Leu	His	Lys	Leu	Pro	Thr	Phe	Leu	Phe	Met	Lys	Arg	Pro	Gly	Pro
			340					345					350		
Asp	Ser	Ser	Pro	Ala	Arg	Ala	Phe	Pro	Pro	Ser	Lys	Ser	Cys	Val	Thr
		355					360					365			
Lys	Pro	Glu	Ala	Thr	Ala	Thr	Ser	Thr	Ser	Pro	Ser	Asn	Phe	Tyr	Gly
	370					375					380				
Asn	Ser	Met	Tyr	Phe	Val	Asn	Pro	Ala	Ser	Ala	Ala	Ser	Lys	Ser	Pro
385					390					395					400
Ala	Gly	Ser	Thr	Pro	Val	Ala	Ile	Pro	Arg	Asp	Phe	Trp	Leu	Arg	Ser
				405					410					415	
Ser	Gly	Arg	Phe	Arg	Gln	Asp	Val	Gln	Glu	Ala	Leu	Glu	Gly	Val	Ser
			420					425					430		
Phe	Ile	Ala	Gln	His	Met	Lys	Asn	Asp	Asp	Glu	Asp	Gln	Ser	Val	Val
		435					440					445			
Glu	Asp	Trp	Lys	Tyr	Val	Ala	Met	Val	Val	Asp	Arg	Leu	Phe	Leu	Trp
	450					455					460				
Val	Phe	Met	Phe	Val	Cys	Val	Leu	Gly	Thr	Val	Gly	Leu	Phe	Leu	Pro
465					470					475					480
Pro	Leu	Phe	Gln	Thr	His	Ala	Ala	Ser	Glu	Gly	Pro	Tyr	Ala	Ala	Gln
				485					490					495	
Arg	Asp														